

**SCORE Search Results Details for Application 10713567 and Search Result us-10-713-567-3\_copy\_7\_77.rag.**

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OM protein - protein search, using sw model

```
Run on:      June 28, 2006, 00:21:43 ; Search time 310 Seconds
              (without alignments)
              104.717 Million cell updates/sec
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Title: US-10-713-567-3\_COPY\_7\_77  
Perfect score: 425  
Sequence: 1 CERDVQCGAGTCCAISLWLR.....TCPCLPNLLCSRFPDGRYRC 71

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 2589679 seqs, 457216429 residues

Total number of hits satisfying chosen parameters: 2589679

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Minimum DB seq length: 0
Maximum DB seq length: 2000000000
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Post-processing: Minimum Match 0%
                  Maximum Match 100%
                  Listing first 45 summaries

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3:  geneseqp2000s:*
4:  geneseqp2001s:*
5:  geneseqp2002s:*
6:  geneseqp2003as:*
7:  geneseqp2003bs:*
8:  geneseqp2004s:*
9:  geneseqp2005s:*
10: geneseqp2006s:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	% Match	Query Length	DB	ID	Description
1	425	100.0	82	9	ADZ88902	Adz88902 Human pro
2	425	100.0	85	5	AAE24393	Aae24393 Human pro
3	425	100.0	85	8	ADS75507	Ads75507 Prokineti
4	425	100.0	86	4	AAB70146	Aab70146 Human G p
5	425	100.0	86	5	ABB76801	Abb76801 Human ZAQ
6	425	100.0	86	5	ABJ05338	Abj05338 Human ZAQ
7	425	100.0	86	5	AAO15529	Aao15529 Human phy
8	425	100.0	86	5	ABB06306	Abb06306 Human G p
9	425	100.0	86	5	AAE24394	Aae24394 Human pro
10	425	100.0	86	5	AAE24383	Aae24383 Human pro
11	425	100.0	86	7	ADD69104	Add69104 Human ZAQ
12	425	100.0	86	7	ADO05360	Ado05360 Human pro
13	425	100.0	86	8	ADN43256	Adn43256 Amino aci
14	425	100.0	86	8	ADR24003	Adr24003 Human ZAQ
15	425	100.0	86	8	ADS86471	Ads86471 Human ZAQ
16	425	100.0	86	8	ADS75508	Ads75508 Prokineti
17	425	100.0	86	8	ADS75494	Ads75494 Human pro
18	425	100.0	86	8	ADS75511	Ads75511 Prokineti
19	425	100.0	86	9	ADW00759	Adw00759 Amino aci
20	425	100.0	86	9	ADZ58575	Adz58575 Human ZAQ
21	425	100.0	86	9	AEB45594	Aeb45594 Human Zve
22	425	100.0	86	9	AED00599	Aed00599 Partial h
23	425	100.0	87	5	AAE24395	Aae24395 Human pro
24	425	100.0	87	8	ADS75509	Ads75509 Prokineti
25	425	100.0	89	5	AAE24392	Aae24392 Human pro
26	425	100.0	89	8	ADS75506	Ads75506 Prokineti
27	425	100.0	105	3	AAZ66745	Aaz66745 Membrane-
28	425	100.0	105	3	AAB18453	Aab18453 A human T
29	425	100.0	105	4	AAB70148	Aab70148 Human G p
30	425	100.0	105	4	AAB68427	Aab68427 Amino aci
31	425	100.0	105	4	AAU12406	Aau12406 Human PRO
32	425	100.0	105	4	AAB53096	Aab53096 Human ang
33	425	100.0	105	4	AAB65268	Aab65268 Human PRO
34	425	100.0	105	4	AAB48175	Aab48175 Human PRO
35	425	100.0	105	4	AAB48067	Aab48067 Human ext
36	425	100.0	105	5	AAM50773	Aam50773 Endocrine
37	425	100.0	105	5	AAU83674	Aau83674 Human PRO
38	425	100.0	105	5	ABB84902	Abb84902 Human PRO
39	425	100.0	105	5	AAO15527	Aao15527 Human phy
40	425	100.0	105	5	ABB06308	Abb06308 Human G p
41	425	100.0	105	5	AAE24382	Aae24382 Human pro
42	425	100.0	105	5	ABB95508	Abb95508 Human ang
43	425	100.0	105	5	ADY31906	Ady31906 Novel hum
44	425	100.0	105	6	ABU58083	Abu58083 Human PRO
45	425	100.0	105	6	ABU59161	Abu59161 Novel hum

## ALIGNMENTS

## RESULT 1

ADZ88902

ID ADZ88902 standard; protein; 82 AA.

XX

AC ADZ88902;

XX

DT 14-JUL-2005 (first entry)

http://es/ScoreAccessWeb/GetItem.action?AppId=10713567&seqId=549046&ItemName=... 7/28/2006

1	425	100.0	105	2	US-09-712-529-5	Sequence 5, Appli
2	425	100.0	105	2	US-10-212-201A-5	Sequence 5, Appli
3	425	100.0	105	2	US-10-212-355-5	Sequence 5, Appli
4	425	100.0	105	2	US-09-991-181-371	Sequence 371, App
5	425	100.0	105	2	US-09-990-444-371	Sequence 371, App
6	425	100.0	105	2	US-09-997-333-371	Sequence 371, App
7	425	100.0	105	2	US-09-992-598-371	Sequence 371, App
8	425	100.0	105	2	US-09-989-735-371	Sequence 371, App
9	425	100.0	105	3	US-09-989-726-371	Sequence 371, App
10	425	100.0	105	3	US-09-997-514-371	Sequence 371, App
11	425	100.0	105	3	US-09-989-728-371	Sequence 371, App
12	425	100.0	105	3	US-09-997-349-371	Sequence 371, App
13	425	100.0	105	3	US-09-997-653-371	Sequence 371, App
14	425	100.0	105	3	US-09-989-293A-371	Sequence 371, App
15	413	97.2	105	2	US-09-621-976-5350	Sequence 5350, Ap
16	330	77.6	80	2	US-09-513-999C-4698	Sequence 4698, Ap
17	264	62.1	108	2	US-09-712-529-2	Sequence 2, Appli
18	264	62.1	108	2	US-10-212-201A-2	Sequence 2, Appli
19	264	62.1	108	2	US-10-212-355-2	Sequence 2, Appli
20	106.5	25.1	224	2	US-09-161-241-14	Sequence 14, Appl
21	102	24.0	186	2	US-09-949-016-7146	Sequence 7146, Ap
22	102	24.0	207	2	US-09-161-241-13	Sequence 13, Appl
23	102	24.0	259	2	US-09-161-241-12	Sequence 12, Appl
24	102	24.0	259	2	US-09-949-016-6872	Sequence 6872, Ap
25	102	24.0	259	2	US-10-012-231A-70	Sequence 70, Appl
26	102	24.0	259	2	US-10-015-389A-70	Sequence 70, Appl
27	102	24.0	259	2	US-10-006-768A-70	Sequence 70, Appl
28	102	24.0	259	2	US-10-015-671A-70	Sequence 70, Appl
29	102	24.0	259	2	US-10-015-393A-70	Sequence 70, Appl
30	102	24.0	259	2	US-10-011-833A-70	Sequence 70, Appl
31	102	24.0	259	2	US-10-006-041A-70	Sequence 70, Appl
32	102	24.0	259	2	US-10-012-064A-70	Sequence 70, Appl
33	102	24.0	259	2	US-10-015-392A-70	Sequence 70, Appl
34	102	24.0	259	3	US-10-011-795B-70	Sequence 70, Appl
35	102	24.0	259	3	US-10-015-386A-70	Sequence 70, Appl
36	102	24.0	259	3	US-10-012-121A-70	Sequence 70, Appl
37	102	24.0	259	3	US-10-006-485A-70	Sequence 70, Appl
38	102	24.0	259	3	US-10-006-746A-70	Sequence 70, Appl
39	102	24.0	259	3	US-10-012-752A-70	Sequence 70, Appl
40	102	24.0	259	3	US-10-017-253A-70	Sequence 70, Appl
41	102	24.0	259	3	US-10-015-519A-70	Sequence 70, Appl
42	102	24.0	259	3	US-10-015-715A-70	Sequence 70, Appl
43	102	24.0	259	3	US-10-007-236A-70	Sequence 70, Appl
44	101	23.8	259	2	US-09-161-241-11	Sequence 11, Appl
45	100.5	23.6	215	2	US-10-104-047-2196	Sequence 2196, Ap

## ALIGNMENTS

## RESULT 1

US-09-712-529-5

; Sequence 5, Application US/09712529

; Patent No. 6485938

; GENERAL INFORMATION:

; APPLICANT: Sheppard, Paul O.

; APPLICANT: Bishop, Paul D.

; APPLICANT: Whitmore, Theodore E.

; APPLICANT: Thompson, Penny P.

; TITLE OF INVENTION: Human Zven Proteins

# SCORE Search Results Details for Application 10713567 and Search Result us-10-713-567-3\_copy\_7\_77.rapbm.

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OM protein - protein search, using sw model

Run on: June 28, 2006, 00:40:02 ; Search time 176.5 Seconds  
(without alignments)  
186.336 Million cell updates/sec

Title: US-10-713-567-3\_COPY\_7\_77  
Perfect score: 425  
Sequence: 1 CERDVQCGAGTCCAISLWLR.....TCPCLPNLLCSRFPDGRYRC 71

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 2097797 seqs, 463214858 residues

Total number of hits satisfying chosen parameters: 2097797

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Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

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- 3: /EMC\_Celerra\_SIDS3/ptodata/2/pubpaa/US09\_PUBCOMB.pep:\*
- 4: /EMC\_Celerra\_SIDS3/ptodata/2/pubpaa/US10A\_PUBCOMB.pep:\*
- 5: /EMC\_Celerra\_SIDS3/ptodata/2/pubpaa/US10B\_PUBCOMB.pep:\*
- 6: /EMC\_Celerra\_SIDS3/ptodata/2/pubpaa/US11\_PUBCOMB.pep:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result	Score	Match	Length	DB	ID	Description
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1	425	100.0	82	5	US-10-977-113-11	Sequence 11, Appl
2	425	100.0	85	4	US-10-016-481-16	Sequence 16, Appl
3	425	100.0	85	4	US-10-323-157-16	Sequence 16, Appl
4	425	100.0	85	5	US-10-713-567-16	Sequence 16, Appl
5	425	100.0	85	5	US-10-811-328-16	Sequence 16, Appl
6	425	100.0	85	5	US-10-912-907-16	Sequence 16, Appl
7	425	100.0	85	5	US-10-415-724-16	Sequence 16, Appl
8	425	100.0	86	4	US-10-016-481-3	Sequence 3, Appli
9	425	100.0	86	4	US-10-016-481-17	Sequence 17, Appl
10	425	100.0	86	4	US-10-323-157-3	Sequence 3, Appli
11	425	100.0	86	4	US-10-323-157-17	Sequence 17, Appl
12	425	100.0	86	4	US-10-417-426-9	Sequence 9, Appli
13	425	100.0	86	4	US-10-333-192-21	Sequence 21, Appl
14	425	100.0	86	5	US-10-680-554-5	Sequence 5, Appli
15	425	100.0	86	5	US-10-713-567-3	Sequence 3, Appli
16	425	100.0	86	5	US-10-713-567-17	Sequence 17, Appl
17	425	100.0	86	5	US-10-713-567-20	Sequence 20, Appl
18	425	100.0	86	5	US-10-811-328-3	Sequence 3, Appli
19	425	100.0	86	5	US-10-811-328-17	Sequence 17, Appl
20	425	100.0	86	5	US-10-811-328-20	Sequence 20, Appl
21	425	100.0	86	5	US-10-912-907-3	Sequence 3, Appli
22	425	100.0	86	5	US-10-912-907-17	Sequence 17, Appl
23	425	100.0	86	5	US-10-415-724-3	Sequence 3, Appli
24	425	100.0	86	5	US-10-415-724-17	Sequence 17, Appl
25	425	100.0	86	5	US-10-871-152-22	Sequence 22, Appl
26	425	100.0	86	5	US-10-503-554A-82	Sequence 82, Appl
27	425	100.0	86	5	US-10-343-095A-117	Sequence 117, App
28	425	100.0	86	6	US-11-073-420-11	Sequence 11, Appl
29	425	100.0	87	4	US-10-016-481-18	Sequence 18, Appl
30	425	100.0	87	4	US-10-323-157-18	Sequence 18, Appl
31	425	100.0	87	5	US-10-713-567-18	Sequence 18, Appl
32	425	100.0	87	5	US-10-811-328-18	Sequence 18, Appl
33	425	100.0	87	5	US-10-912-907-18	Sequence 18, Appl
34	425	100.0	87	5	US-10-415-724-18	Sequence 18, Appl
35	425	100.0	89	4	US-10-016-481-15	Sequence 15, Appl
36	425	100.0	89	4	US-10-323-157-15	Sequence 15, Appl
37	425	100.0	89	5	US-10-713-567-15	Sequence 15, Appl
38	425	100.0	89	5	US-10-811-328-15	Sequence 15, Appl
39	425	100.0	89	5	US-10-912-907-15	Sequence 15, Appl
40	425	100.0	89	5	US-10-415-724-15	Sequence 15, Appl
41	425	100.0	105	3	US-09-989-722-371	Sequence 371, App
42	425	100.0	105	3	US-09-989-723-371	Sequence 371, App
43	425	100.0	105	3	US-09-989-279-371	Sequence 371, App
44	425	100.0	105	3	US-09-989-727-371	Sequence 371, App
45	425	100.0	105	3	US-09-989-731-371	Sequence 371, App

## ALIGNMENTS

## RESULT 1

US-10-977-113-11

; Sequence 11, Application US/10977113

; Publication No. US20050143287A1

; GENERAL INFORMATION:

; APPLICANT: Zhou, Qun-Yong

; TITLE OF INVENTION: Primate Prokineticin and Prokineticin

; TITLE OF INVENTION: Receptor Polypeptides, Related Compositions and Methods

; FILE REFERENCE: 66778-377

; CURRENT APPLICATION NUMBER: US/10/977,113

; CURRENT FILING DATE: 2004-10-29

# SCORE Search Results Details for Application 10713567 and Search Result us-10-713-567- 3\_copy\_7\_77.rapbn.

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<a href="#">Page</a>	<a href="#">List</a>	<a href="#">Overview</a>	<a href="#">FAQ</a>	<a href="#">Suggestions</a>

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OM protein - protein search, using sw model

Run on: June 28, 2006, 00:41:22 ; Search time 12 Seconds  
(without alignments)  
135.170 Million cell updates/sec

Title: US-10-713-567-3\_COPY\_7\_77  
Perfect score: 425  
Sequence: 1 CERDVQCGAGTCCAISLWLR.....TCPCLPNLLCSRFPDGRYRC 71

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 99297 seqs, 22845552 residues

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Maximum DB seq length: 2000000000

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Maximum Match 100%  
Listing first 45 summaries

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- 3: /EMC\_Celerra\_SIDS3/ptodata/1/pubpaa/US07\_NEW\_PUB.pep:\*
- 4: /EMC\_Celerra\_SIDS3/ptodata/1/pubpaa/US08\_NEW\_PUB.pep:\*
- 5: /EMC\_Celerra\_SIDS3/ptodata/1/pubpaa/PCT\_NEW\_PUB.pep:\*
- 6: /EMC\_Celerra\_SIDS3/ptodata/1/pubpaa/US10\_NEW\_PUB.pep:\*
- 7: /EMC\_Celerra\_SIDS3/ptodata/1/pubpaa/US11\_NEW\_PUB.pep:\*
- 8: /EMC\_Celerra\_SIDS3/ptodata/1/pubpaa/US60\_NEW\_PUB.pep:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

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Result	Query

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1	425	100.0	86	7	US-11-304-129-21	Sequence 21, Appl
2	425	100.0	105	7	US-11-304-129-23	Sequence 23, Appl
3	424	99.8	86	7	US-11-304-129-20	Sequence 20, Appl
4	424	99.8	105	7	US-11-304-129-22	Sequence 22, Appl
5	288	67.8	80	7	US-11-304-129-34	Sequence 34, Appl
6	102	24.0	259	6	US-10-196-749-250	Sequence 250, App
7	101	23.8	272	7	US-11-197-665-4	Sequence 4, Appli
8	100.5	23.6	350	7	US-11-101-316-8	Sequence 8, Appli
9	97	22.8	266	6	US-10-505-928-533	Sequence 533, App
10	97	22.8	266	7	US-11-197-665-2	Sequence 2, Appli
11	75.5	17.8	446	7	US-11-293-697-3580	Sequence 3580, Ap
12	72.5	17.1	425	7	US-11-293-697-4381	Sequence 4381, Ap
13	67.5	15.9	909	6	US-10-449-902-44686	Sequence 44686, A
14	67	15.8	491	7	US-11-217-997-30	Sequence 30, Appl
15	67	15.8	1398	7	US-11-217-997-4	Sequence 4, Appli
16	67	15.8	1403	7	US-11-217-997-12	Sequence 12, Appl
17	67	15.8	1404	7	US-11-217-997-2	Sequence 2, Appli
18	67	15.8	1547	7	US-11-217-997-22	Sequence 22, Appl
19	67	15.8	1577	7	US-11-217-997-16	Sequence 16, Appl
20	67	15.8	1577	7	US-11-217-997-20	Sequence 20, Appl
21	67	15.8	1594	7	US-11-217-997-18	Sequence 18, Appl
22	67	15.8	1620	7	US-11-217-997-42	Sequence 42, Appl
23	67	15.8	1653	7	US-11-217-997-40	Sequence 40, Appl
24	66	15.5	85	6	US-10-525-126-295	Sequence 295, App
25	65.5	15.4	92	6	US-10-449-902-41737	Sequence 41737, A
26	65	15.3	575	7	US-11-217-997-32	Sequence 32, Appl
27	65	15.3	1418	7	US-11-217-997-38	Sequence 38, Appl
28	65	15.3	1450	7	US-11-217-997-6	Sequence 6, Appli
29	64.5	15.2	342	7	US-11-038-753-1	Sequence 1, Appli
30	64.5	15.2	355	6	US-10-504-973-33	Sequence 33, Appl
31	64.5	15.2	461	6	US-10-511-937-2945	Sequence 2945, Ap
32	64.5	15.2	461	7	US-11-183-218-32	Sequence 32, Appl
33	63.5	14.9	172	6	US-10-449-902-48116	Sequence 48116, A
34	63	14.8	243	7	US-11-320-192-9	Sequence 9, Appli
35	62	14.6	243	7	US-11-320-192-12	Sequence 12, Appl
36	62	14.6	1198	7	US-11-217-997-14	Sequence 14, Appl
37	61.5	14.5	277	6	US-10-511-937-2455	Sequence 2455, Ap
38	61	14.4	569	6	US-10-449-902-46970	Sequence 46970, A
39	61	14.4	729	7	US-11-175-714-8	Sequence 8, Appli
40	60	14.1	720	7	US-11-175-714-4	Sequence 4, Appli
41	60	14.1	734	7	US-11-238-282-19	Sequence 19, Appl
42	60	14.1	3934	7	US-11-165-586-20	Sequence 20, Appl
43	59	13.9	454	6	US-10-449-902-33449	Sequence 33449, A
44	59	13.9	454	6	US-10-449-902-44623	Sequence 44623, A
45	59	13.9	713	7	US-11-175-714-5	Sequence 5, Appli

## ALIGNMENTS

## RESULT 1

US-11-304-129-21

; Sequence 21, Application US/11304129

; Publication No. US20060088915A1

; GENERAL INFORMATION:

; APPLICANT: OHTAKI, Tetsuya

; APPLICANT: MASUDA, Yasushi

; APPLICANT: TAKATSU, Yoshihiro

; APPLICANT: WATANABE, Takuya



**SCORE Search Re**

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This page gives you Search Results detail for the Application 10713567 and Search Result us-10-7:  
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OM protein - protein search, using sw model.

Run on: June 28, 2006, 00:32:53 ; Search time 24 Seconds  
(without alignments)  
284.641 Million cell updates/sec

Title: US-10-713-567-3\_COPY\_7\_77  
Perfect score: 425  
Sequence: 1 CERDVQCGAGTCCAISLWLR.....TCPCLPNLLCSRFPDGRYRC 71

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : PIR\_80:\*  
1: pir1:\*  
2: pir2:\*  
3: pir3:\*  
4: pir4:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	100.5	23.6	350	2	JC7188	REIC protein - hum
2	82.5	19.4	640	2	T08179	LRG5 protein - Ch1
3	81	19.1	1964	2	T09059	notch4 - mouse
4	77.5	18.2	473	2	A56175	adhesive plaque pr
5	73	17.2	2531	2	T31070	notch homolog - se
6	71.5	16.8	1178	1	A39804	thrombospondin pre
7	71	16.7	112	2	I51909	colipase precursor
8	71	16.7	286	2	S34665	collagen, cuticula

9	70.5	16.6	591	2	I48141	acrogranin - guine
10	70.5	16.6	2318	2	S45306	notch 3 protein -
11	70	16.5	112	1	XLHU	colipase precursor
12	69	16.2	593	1	GYHU	granulin precursor
13	68.5	16.1	850	2	T14450	serine/threonine k
14	68.5	16.1	1172	2	A42587	thrombospondin 2 p
15	68	16.0	547	2	A33901	mannosyl-oligosacc
16	68	16.0	601	2	B36346	fibulin 1 precurs
17	68	16.0	683	2	C36346	fibulin 1 precurs
18	68	16.0	1101	2	T16840	hypothetical prote
19	68	16.0	1150	2	A41641	mannosyl-oligosacc
20	68	16.0	5147	1	IJFFTM	cadherin-related t
21	67	15.8	237	2	S45463	probable membrane
22	67	15.8	2215	2	T00348	LR11 protein - mou
23	66.5	15.6	1376	2	G00043	osteonidogen - hum
24	66	15.5	1172	1	TSHUP2	thrombospondin 2 p
25	65.5	15.4	251	2	A55035	cysteine-rich prot
26	65.5	15.4	802	2	T24293	hypothetical prote
27	65.5	15.4	949	2	T24294	hypothetical prote
28	65	15.3	112	2	A46717	colipase precursor
29	64.5	15.2	191	2	H71370	hypothetical prote
30	64.5	15.2	461	1	A35356	tumor necrosis fac
31	64.5	15.2	1574	2	T13954	MEGF6 protein - ra
32	64	15.1	117	2	H72706	hypothetical prote
33	64	15.1	217	2	A98196	hypothetical prote
34	64	15.1	225	2	A86043	probable transposa
35	64	15.1	589	2	C38128	epithelin/granulin
36	64	15.1	1143	2	T22952	hypothetical prote
37	64	15.1	3133	2	S52093	hemocytin - silkwo
38	63.5	14.9	1847	2	T18308	probable vitellog
39	63	14.8	589	2	B38128	epithelin/granulin
40	63	14.8	2321	2	S78549	notch3 protein - h
41	63	14.8	2871	2	A55567	fibrillin I - bovi
42	62.5	14.7	360	2	AH2272	fructose-bisphosph
43	62.5	14.7	895	1	IJXLCP	EP-cadherin precu
44	62.5	14.7	1984	2	T13171	probable vitellog
45	62	14.6	4545	1	S25111	alpha-2-macroglobu

## ALIGNMENTS

## RESULT 1

JC7188

REIC protein - human

C;Species: Homo sapiens (man)

C;Date: 04-Mar-2000 #sequence\_revision 04-Mar-2000 #text\_change 11-May-2000

C;Accession: JC7188

R;Tsugi, T.; Miyazaki, M.; Sakaguchi, M.; Inoue, Y.; Namba, M.

Biochem. Biophys. Res. Commun. 268, 20-24, 2000

A;Title: A REIC gene shows down-regulation in human immortalized cells and human tumor

A;Reference number: JC7188; MUID:20119095; PMID:10652205

A;Accession: JC7188

A;Molecule type: mRNA

A;Residues: 1-350

A;Cross-references: UNIPARC:UPI0000179471; DDBJ:AB034203

A;Experimental source: heart

C;Comment: This protein is a secreted glycoprotein for head induction in amphibian emb

C;Genetics:

A;Gene: reic

C;Superfamily: human REIC protein

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OM protein - protein search, using sw model

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Run on:      June 28, 2006, 00:22:07 ; Search time 191 Seconds
              (without alignments)
              343.854 Million cell updates/sec
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Title: US-10-713-567-3\_COPY\_7\_77  
Perfect score: 425  
Sequence: 1 CERDVOCGAGTCCAISLWLR.....TCPCLPNLLCSRFPDGRYRC 71

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 2849598 seqs, 925015592 residues

Total number of hits satisfying chosen parameters: 2849598

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Minimum DB seq length: 0
Maximum DB seq length: 2000000000
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Post-processing: Minimum Match 0%
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                  Listing first 45 summaries
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2:  uniprot_trembl:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query		DB	ID	Description
		Match	Length			
1	425	100.0	105	1	PROK1_HUMAN	P58294 homo sapien
2	425	100.0	105	2	Q5VWD4_HUMAN	Q5vwd4 homo sapien
3	424	99.8	105	2	Q8TC69_HUMAN	Q8tc69 homo sapien
4	406	95.5	105	1	PROK1_RAT	Q8r414 rattus norv

5	399	93.9	81	2	Q8K457_MOUSE	Q8k457 mus musculu
6	378	88.9	81	2	Q3ZFI2_BOVIN	Q3zfi2 bos taurus
7	306	72.0	104	2	Q2XXR8_VARVA	Q2xxr8 varanus var
8	301	70.8	104	2	Q2XXR7_VARVA	Q2xxr7 varanus var
9	288	67.8	81	1	VPRA_DENPO	P25687 dendroaspis
10	277	65.2	108	2	Q863H4_BOVIN	Q863h4 bos taurus
11	268	63.1	106	2	Q4RVU3_TETNG	Q4rvu3 tetraodon n
12	264	62.1	108	2	Q6ISR0_HUMAN	Q6isr0 homo sapien
13	259	60.9	107	1	PROK2_RAT	Q8r413 rattus norv
14	259	60.9	107	2	Q50E37_9MURI	Q50e37 arvicanthis
15	259	60.9	107	2	Q50E38_9MURI	Q50e38 arvicanthis
16	258	60.7	102	2	Q4SR12_TETNG	Q4sr12 tetraodon n
17	257	60.5	128	2	Q863H5_BOVIN	Q863h5 bos taurus
18	247.5	58.2	96	2	Q8JFQ0_BOMMX	Q8jfq0 bombina max
19	243.5	57.3	129	1	PROK2_HUMAN	Q9hc23 homo sapien
20	243.5	57.3	129	2	Q53Z79_HUMAN	Q53z79 homo sapien
21	242.5	57.1	96	2	Q5W280_BOMOR	Q5w280 bombina ori
22	238.5	56.1	128	1	PROK2_MOUSE	Q9qxu7 mus musculu
23	238.5	56.1	128	2	Q50E33_9MURI	Q50e33 arvicanthis
24	238.5	56.1	128	2	Q50E34_9MURI	Q50e34 arvicanthis
25	238.5	56.1	128	2	Q6V8J7_RAT	Q6v8j7 rattus norv
26	236.5	55.6	96	1	BV8_BOMVA	Q9pw66 bombina var
27	227.5	53.5	96	2	Q8JFE6_BOMMX	Q8jfe6 bombina max
28	226.5	53.3	96	2	Q8JFX8_BOMMX	Q8jfx8 bombina max
29	226.5	53.3	96	2	Q8JFY1_BOMMX	Q8jfy1 bombina max
30	225	52.9	96	2	Q8JFY0_BOMMX	Q8jfy0 bombina max
31	222.5	52.4	96	2	Q8JFX9_BOMMX	Q8jfx9 bombina max
32	222.5	52.4	96	2	Q8JFY2_BOMMX	Q8jfy2 bombina max
33	164	38.6	82	2	Q2TBS7_BOVIN	Q2tbs7 bos taurus
34	161	37.9	86	2	Q50E35_9MURI	Q50e35 arvicanthis
35	161	37.9	86	2	Q50E36_9MURI	Q50e36 arvicanthis
36	154	36.2	39	2	Q50E61_9MURI	Q50e61 arvicanthis
37	117.5	27.6	124	2	Q56R10_PENMO	Q56r10 penaeus mon
38	112	26.4	96	2	Q8UUX3_CHICK	Q8uux3 gallus gall
39	107.5	25.3	221	1	DKK4_MOUSE	Q8vej3 mus musculu
40	107.5	25.3	350	1	DKK3_CHICK	Q90839 gallus gall
41	106.5	25.1	224	1	DKK4_HUMAN	Q9ubt3 homo sapien
42	106.5	25.1	224	2	Q3KNX0_HUMAN	Q3knx0 homo sapien
43	104	24.5	255	2	Q9DDA4_XENLA	Q9dda4 xenopus lae
44	102	24.0	259	1	DKK2_HUMAN	Q9ubu2 homo sapien
45	101	23.8	259	1	DKK2_MOUSE	Q9qyz8 mus musculu

## ALIGNMENTS

## RESULT 1

## PROK1\_HUMAN

ID PROK1\_HUMAN STANDARD; PRT; 105 AA.

AC P58294;

DT 26-SEP-2001, integrated into UniProtKB/Swiss-Prot.

DT 26-SEP-2001, sequence version 1.

DT 21-FEB-2006, entry version 35.

DE Prokineticin-1 precursor (Endocrine-gland-derived vascular endothelial growth factor) (EG-VEGF) (Mambakine).

GN Name=PROK1; ORFNames=UNQ600/PRO1186;

OS Homo sapiens (Human).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;

OC Homo.

OX NCBI\_TaxID=9606;

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OM protein - protein search, using sw model

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Run on:      June 28, 2006, 00:21:43 ; Search time 310 Seconds
              (without alignments)
              104.717 Million cell updates/sec
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Perfect score: 416
Sequence:      1 CDKDSQCGGGMCCAVSIWVK.....TCPCLPGLACLRTSFNRFIC 71
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Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 2589679 seqs, 457216429 residues

Total number of hits satisfying chosen parameters: 2589679

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Minimum DB seq length: 0
Maximum DB seq length: 2000000000
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Post-processing: Minimum Match 0%
                  Maximum Match 100%
                  Listing first 45 summaries
```

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1:  geneseqp1980s:*
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3:  geneseqp2000s:*
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6:  geneseqp2003as:*
7:  geneseqp2003bs:*
8:  geneseqp2004s:*
9:  geneseqp2005s:*
10: geneseqp2006s:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	% Match	Query Length	DB	ID	Description
1	416	100.0	80	5	ABG94400	Abg94400 C-termina
2	416	100.0	80	7	ADD69044	Add69044 Human Bv8
3	416	100.0	81	5	ABG94398	Abg94398 Human GPC
4	416	100.0	81	5	AAO15530	Aao15530 Human phy
5	416	100.0	81	5	AAE24385	Aae24385 Human pro
6	416	100.0	81	7	ADD69041	Add69041 Human Bv8
7	416	100.0	81	7	ADO05356	Ado05356 Human maj
8	416	100.0	81	8	ADN43258	Adn43258 Amino aci
9	416	100.0	81	8	ADR24005	Adr24005 Human ZAQ
10	416	100.0	81	8	ADS86493	Ads86493 Human BV8
11	416	100.0	81	8	ADS75497	Ads75497 Human pro
12	416	100.0	81	9	ADW00755	Adw00755 Amino aci
13	416	100.0	81	9	ADZ88900	Adz88900 Human pro
14	416	100.0	81	9	ADZ58574	Adz58574 Human ZAQ
15	416	100.0	81	9	AEB45593	Aeb45593 Human Zve
16	416	100.0	81	9	AED00597	Aed00597 Human pro
17	416	100.0	100	9	ADY86166	Ady86166 Human Bv8
18	416	100.0	108	4	AAB68426	Aab68426 Amino aci
19	416	100.0	108	5	ABG94397	Abg94397 Human GPC
20	416	100.0	108	5	AAO15531	Aao15531 Human phy
21	416	100.0	108	5	AAE24384	Aae24384 Human pro
22	416	100.0	108	6	ABU07602	Abu07602 Human ZVE
23	416	100.0	108	6	AAE36789	Aae36789 Human Bv8
24	416	100.0	108	7	ADD69039	Add69039 Human Bv8
25	416	100.0	108	7	ADF28067	Adf28067 Human Zve
26	416	100.0	108	7	ABG75087	Abg75087 Human pro
27	416	100.0	108	7	ADJ71811	Adj71811 Human pro
28	416	100.0	108	8	ADN41839	Adn41839 Amino aci
29	416	100.0	108	8	ADO24421	Ado24421 Human PRO
30	416	100.0	108	8	ADS86957	Ads86957 Human Zve
31	416	100.0	108	8	ADS00460	Ads00460 Human Bv8
32	416	100.0	108	8	ADS86495	Ads86495 Human BV8
33	416	100.0	108	8	ADS75496	Ads75496 Human pro
34	416	100.0	108	9	AEA23706	Aea23706 Human PRO
35	416	100.0	108	9	AEB45585	Aeb45585 Human Zve
36	416	100.0	108	9	AED08085	Aed08085 Human Zve
37	416	100.0	116	8	ADN41861	Adn41861 Amino aci
38	416	100.0	116	8	ADS86981	Ads86981 Human Zve
39	409	98.3	108	9	ADZ88897	Adz88897 Rhesus mo
40	409	98.3	108	9	AED00594	Aed00594 Rhesus mo
41	404	97.1	80	9	ADZ88901	Adz88901 Mouse pro
42	404	97.1	80	9	AED00598	Aed00598 Mouse/rat
43	404	97.1	81	5	ABG94402	Abg94402 Rat GPCR
44	404	97.1	81	5	ABB06963	Abb06963 Rat G pro
45	404	97.1	81	7	ADD69061	Add69061 Rat Bv8-r

## ALIGNMENTS

## RESULT 1

ABG94400

ID ABG94400 standard; protein; 80 AA.

XX

AC ABG94400;

XX

DT 27-NOV-2002 (first entry)

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OM protein - protein search, using sw model

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Run on:      June 28, 2006, 00:39:12 ; Search time 36 Seconds
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Sequence: 1 CDKDSQCGGGMCCAVSIWVK.....TCPCLPGLACLRTSFNRFIC 71

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result		Query				Description	
No.	Score	Match	Length	DB	ID		

1	416	100.0	108	2	US-09-712-529-2	Sequence 2, Appli
2	416	100.0	108	2	US-10-212-201A-2	Sequence 2, Appli
3	416	100.0	108	2	US-10-212-355-2	Sequence 2, Appli
4	264	63.5	105	2	US-09-712-529-5	Sequence 5, Appli
5	264	63.5	105	2	US-10-212-201A-5	Sequence 5, Appli
6	264	63.5	105	2	US-10-212-355-5	Sequence 5, Appli
7	264	63.5	105	2	US-09-991-181-371	Sequence 371, App
8	264	63.5	105	2	US-09-990-444-371	Sequence 371, App
9	264	63.5	105	2	US-09-997-333-371	Sequence 371, App
10	264	63.5	105	2	US-09-992-598-371	Sequence 371, App
11	264	63.5	105	2	US-09-989-735-371	Sequence 371, App
12	264	63.5	105	3	US-09-989-726-371	Sequence 371, App
13	264	63.5	105	3	US-09-997-514-371	Sequence 371, App
14	264	63.5	105	3	US-09-989-728-371	Sequence 371, App
15	264	63.5	105	3	US-09-997-349-371	Sequence 371, App
16	264	63.5	105	3	US-09-997-653-371	Sequence 371, App
17	264	63.5	105	3	US-09-989-293A-371	Sequence 371, App
18	257	61.8	105	2	US-09-621-976-5350	Sequence 5350, Ap
19	229	55.0	80	2	US-09-513-999C-4698	Sequence 4698, Ap
20	100.5	24.2	224	2	US-09-161-241-14	Sequence 14, Appl
21	100	24.0	266	2	US-09-161-241-10	Sequence 10, Appl
22	100	24.0	266	2	US-09-976-594-1086	Sequence 1086, Ap
23	100	24.0	266	2	US-09-999-833A-456	Sequence 456, App
24	100	24.0	266	2	US-10-020-445A-456	Sequence 456, App
25	100	24.0	266	2	US-09-978-189-456	Sequence 456, App
26	100	24.0	266	2	US-10-017-085A-456	Sequence 456, App
27	100	24.0	266	3	US-10-145-129A-456	Sequence 456, App
28	100	24.0	266	3	US-10-013-929A-456	Sequence 456, App
29	100	24.0	266	3	US-10-013-917A-456	Sequence 456, App
30	98	23.6	259	2	US-09-161-241-11	Sequence 11, Appl
31	97	23.3	186	2	US-09-949-016-7146	Sequence 7146, Ap
32	97	23.3	207	2	US-09-161-241-13	Sequence 13, Appl
33	97	23.3	259	2	US-09-161-241-12	Sequence 12, Appl
34	97	23.3	259	2	US-09-949-016-6872	Sequence 6872, Ap
35	97	23.3	259	2	US-10-012-231A-70	Sequence 70, Appl
36	97	23.3	259	2	US-10-015-389A-70	Sequence 70, Appl
37	97	23.3	259	2	US-10-006-768A-70	Sequence 70, Appl
38	97	23.3	259	2	US-10-015-671A-70	Sequence 70, Appl
39	97	23.3	259	2	US-10-015-393A-70	Sequence 70, Appl
40	97	23.3	259	2	US-10-011-833A-70	Sequence 70, Appl
41	97	23.3	259	2	US-10-006-041A-70	Sequence 70, Appl
42	97	23.3	259	2	US-10-012-064A-70	Sequence 70, Appl
43	97	23.3	259	2	US-10-015-392A-70	Sequence 70, Appl
44	97	23.3	259	3	US-10-011-795B-70	Sequence 70, Appl
45	97	23.3	259	3	US-10-015-386A-70	Sequence 70, Appl

## ALIGNMENTS

## RESULT 1

US-09-712-529-2

; Sequence 2, Application US/09712529

; Patent No. 6485938

; GENERAL INFORMATION:

; APPLICANT: Sheppard, Paul O.

; APPLICANT: Bishop, Paul D.

; APPLICANT: Whitmore, Theodore E.

; APPLICANT: Thompson, Penny P.

; TITLE OF INVENTION: Human Zven Proteins



http://es/ScoreAccessWeb/GetItem.action?AppId=10713567&seqId=549053&ItemName=... 7/28/2006

1	416	100.0	80	4	US-10-467-019-22	Sequence 22, Appl
2	416	100.0	80	5	US-10-503-554A-22	Sequence 22, Appl
3	416	100.0	81	4	US-10-016-481-6	Sequence 6, Appli
4	416	100.0	81	4	US-10-323-157-6	Sequence 6, Appli
5	416	100.0	81	4	US-10-417-426-5	Sequence 5, Appli
6	416	100.0	81	4	US-10-467-019-19	Sequence 19, Appl
7	416	100.0	81	5	US-10-680-554-7	Sequence 7, Appli
8	416	100.0	81	5	US-10-713-567-6	Sequence 6, Appli
9	416	100.0	81	5	US-10-811-328-6	Sequence 6, Appli
10	416	100.0	81	5	US-10-912-907-6	Sequence 6, Appli
11	416	100.0	81	5	US-10-415-724-6	Sequence 6, Appli
12	416	100.0	81	5	US-10-977-113-9	Sequence 9, Appli
13	416	100.0	81	5	US-10-871-152-18	Sequence 18, Appl
14	416	100.0	81	5	US-10-503-554A-19	Sequence 19, Appl
15	416	100.0	81	6	US-11-073-420-9	Sequence 9, Appli
16	416	100.0	100	3	US-09-886-242A-4	Sequence 4, Appli
17	416	100.0	100	4	US-10-027-603-4	Sequence 4, Appli
18	416	100.0	100	5	US-10-692-299-4	Sequence 4, Appli
19	416	100.0	108	4	US-10-016-481-5	Sequence 5, Appli
20	416	100.0	108	4	US-10-231-411-4	Sequence 4, Appli
21	416	100.0	108	4	US-10-212-355-2	Sequence 2, Appli
22	416	100.0	108	4	US-10-323-157-5	Sequence 5, Appli
23	416	100.0	108	4	US-10-212-201-2	Sequence 2, Appli
24	416	100.0	108	4	US-10-467-019-17	Sequence 17, Appl
25	416	100.0	108	4	US-10-680-755A-2	Sequence 2, Appli
26	416	100.0	108	4	US-10-680-800A-2	Sequence 2, Appli
27	416	100.0	108	5	US-10-713-567-5	Sequence 5, Appli
28	416	100.0	108	5	US-10-811-328-5	Sequence 5, Appli
29	416	100.0	108	5	US-10-912-907-5	Sequence 5, Appli
30	416	100.0	108	5	US-10-415-724-5	Sequence 5, Appli
31	416	100.0	108	5	US-10-990-246-2	Sequence 2, Appli
32	416	100.0	108	5	US-10-503-554A-17	Sequence 17, Appl
33	416	100.0	108	5	US-10-982-168-2	Sequence 2, Appli
34	416	100.0	108	5	US-10-504-588-6	Sequence 6, Appli
35	416	100.0	116	4	US-10-680-755A-26	Sequence 26, Appl
36	416	100.0	116	4	US-10-680-800A-26	Sequence 26, Appl
37	409	98.3	81	6	US-11-073-420-37	Sequence 37, Appl
38	409	98.3	108	5	US-10-713-567-34	Sequence 34, Appl
39	409	98.3	108	5	US-10-977-113-6	Sequence 6, Appli
40	409	98.3	108	6	US-11-073-420-6	Sequence 6, Appli
41	404	97.1	80	5	US-10-977-113-10	Sequence 10, Appl
42	404	97.1	80	6	US-11-073-420-10	Sequence 10, Appl
43	404	97.1	81	4	US-10-417-426-7	Sequence 7, Appli
44	404	97.1	81	4	US-10-467-019-39	Sequence 39, Appl
45	404	97.1	81	4	US-10-362-504-71	Sequence 71, Appl

## ALIGNMENTS

## RESULT 1

US-10-467-019-22

; Sequence 22, Application US/10467019

; Publication No. US20040048314A1

; GENERAL INFORMATION:

; APPLICANT: Takeda Chemical Industries, Ltd.

; TITLE OF INVENTION: No. US20040048314A1el Physiological Active Peptide and Its Use

; FILE REFERENCE: P01-0295PCT

; CURRENT APPLICATION NUMBER: US/10/467,019

; CURRENT FILING DATE: 2003-08-01

; PRIOR APPLICATION NUMBER: JP2001-026820

Comments /  
Suggestions

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http://es/ScoreAccessWeb/GetItem.action?AppId=10713567&seqId=549054&ItemName=... 7/28/2006

No.	Score	Match	Length	DB	ID	Description
1	289	69.5	80	7	US-11-304-129-34	Sequence 34, Appl
2	264	63.5	86	7	US-11-304-129-21	Sequence 21, Appl
3	264	63.5	105	7	US-11-304-129-23	Sequence 23, Appl
4	263	63.2	86	7	US-11-304-129-20	Sequence 20, Appl
5	263	63.2	105	7	US-11-304-129-22	Sequence 22, Appl
6	103	24.8	272	7	US-11-197-665-4	Sequence 4, Appli
7	100	24.0	266	6	US-10-505-928-533	Sequence 533, App
8	100	24.0	266	7	US-11-197-665-2	Sequence 2, Appli
9	97	23.3	259	6	US-10-196-749-250	Sequence 250, App
10	95	22.8	350	7	US-11-101-316-8	Sequence 8, Appli
11	70.5	16.9	575	7	US-11-217-997-32	Sequence 32, Appl
12	70.5	16.9	1418	7	US-11-217-997-38	Sequence 38, Appl
13	70.5	16.9	1450	7	US-11-217-997-6	Sequence 6, Appli
14	70.5	16.9	1547	7	US-11-217-997-22	Sequence 22, Appl
15	70.5	16.9	1577	7	US-11-217-997-16	Sequence 16, Appl
16	70.5	16.9	1577	7	US-11-217-997-20	Sequence 20, Appl
17	70.5	16.9	1620	7	US-11-217-997-42	Sequence 42, Appl
18	70.5	16.9	1653	7	US-11-217-997-40	Sequence 40, Appl
19	67	16.1	1594	7	US-11-217-997-18	Sequence 18, Appl
20	66.5	16.0	1398	7	US-11-217-997-4	Sequence 4, Appli
21	66.5	16.0	1403	7	US-11-217-997-12	Sequence 12, Appli
22	66.5	16.0	1404	7	US-11-217-997-2	Sequence 2, Appli
23	66	15.9	69	6	US-10-953-349-31815	Sequence 31815, A
24	66	15.9	81	6	US-10-953-349-31814	Sequence 31814, A
25	66	15.9	5738	6	US-10-505-928-150	Sequence 150, App
26	62.5	15.0	2026	6	US-10-505-928-831	Sequence 831, App
27	62	14.9	491	7	US-11-217-997-30	Sequence 30, Appl
28	61.5	14.8	686	7	US-11-175-714-25	Sequence 25, Appl
29	61.5	14.8	686	7	US-11-175-714-40	Sequence 40, Appl
30	61.5	14.8	686	7	US-11-175-714-42	Sequence 42, Appl
31	61.5	14.8	686	7	US-11-175-714-44	Sequence 44, Appl
32	61.5	14.8	686	7	US-11-175-714-46	Sequence 46, Appl
33	60.5	14.5	446	7	US-11-293-697-3580	Sequence 3580, Ap
34	60.5	14.5	1182	6	US-10-449-902-41231	Sequence 41231, A
35	60	14.4	1238	7	US-11-178-724-22	Sequence 22, Appl
36	59.5	14.3	1198	7	US-11-217-997-14	Sequence 14, Appl
37	59.5	14.3	1218	7	US-11-178-724-21	Sequence 21, Appl
38	59	14.2	1674	6	US-10-511-937-2587	Sequence 2587, Ap
39	58.5	14.1	282	6	US-10-953-349-19704	Sequence 19704, A
40	58.5	14.1	309	6	US-10-953-349-19703	Sequence 19703, A
41	58.5	14.1	335	6	US-10-953-349-19702	Sequence 19702, A
42	58.5	14.1	340	6	US-10-449-902-31539	Sequence 31539, A
43	58	13.9	102	6	US-10-953-349-26524	Sequence 26524, A
44	58	13.9	756	6	US-10-449-902-44363	Sequence 44363, A
45	57.5	13.8	97	6	US-10-196-749-468	Sequence 468, App

## ALIGNMENTS

## RESULT 1

US-11-304-129-34

; Sequence 34, Application US/11304129

; Publication No. US20060088915A1

; GENERAL INFORMATION:

; APPLICANT: OHTAKI, Tetsuya

; APPLICANT: MASUDA, Yasushi

; APPLICANT: TAKATSU, Yoshihiro

; APPLICANT: WATANABE, Takuya

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This page gives you Search Results detail for the Application 10713567 and Search Result us-10-7:  
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OM protein - protein search, using sw model

Run on: June 28, 2006, 00:32:53 ; Search time 24 Seconds  
(without alignments)  
284.641 Million cell updates/sec

Title: US-10-713-567-6\_COPY\_7\_77  
Perfect score: 416  
Sequence: 1 CDKDSQCGGGMCCAIVSIWVK.....TCPCLPGLACLRTSFNRFIC 71

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : PIR\_80:\*  
1: pir1:\*  
2: pir2:\*  
3: pir3:\*  
4: pir4:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	% Match	Query Length	ID	Description
1	95	22.8	350	2 JC7188	REIC protein - hum
2	76.5	18.4	1574	2 T13954	MEGF6 protein - ra
3	71.5	17.2	264	2 T16271	hypothetical prote
4	69.5	16.7	2471	2 A49128	cell-fate determin
5	68	16.3	313	2 S08198	cytochrome-c3 hydr
6	68	16.3	1609	1 MMHUB2	laminin gamma-1 ch
7	67	16.1	314	1 HQDVSG	cytochrome-c3 hydr
8	66	15.9	3712	2 S18253	laminin alpha-1 ch

9	65.5	15.7	1620	2	T27283	hypothetical prote
10	65.5	15.7	2195	2	T34264	hypothetical prote
11	65	15.6	112	1	XLHU	colipase precursor
12	65	15.6	4135	2	T42629	tenascin-X - bovin
13	64	15.4	1955	1	AGCH	agrin precursor -
14	63.5	15.3	1687	2	T30176	EGF repeat transme
15	63	15.1	112	2	I51909	colipase precursor
16	63	15.1	1522	2	H88380	protein T22F7.3 [i
17	63	15.1	3566	1	A40701	tenascin-X precurs
18	63	15.1	13288	2	T03099	mucin, submaxillar
19	62.5	15.0	109	2	S67091	probable membrane
20	62	14.9	250	1	A49053	CD27 antigen precu
21	62	14.9	297	2	H69609	hypothetical prote
22	62	14.9	1722	2	E89753	protein F11C7.4 [i
23	61.5	14.8	203	2	H75434	hypothetical prote
24	61.5	14.8	318	2	E87929	protein T22H2.6 [i
25	61.5	14.8	345	2	T25138	hypothetical prote
26	61.5	14.8	358	2	T25137	hypothetical prote
27	61.5	14.8	686	2	JC7569	Delta-4 protein -
28	61.5	14.8	3871	2	T22812	hypothetical prote
29	61	14.7	191	2	H71370	hypothetical prote
30	61	14.7	237	2	S45463	probable membrane
31	61	14.7	1984	2	T13171	probable vitellog
32	61	14.7	2098	2	T18397	protein CTRP - mal
33	60.5	14.5	284	2	S17820	protoporphyrin IX
34	60.5	14.5	317	1	A45865	cytochrome-c3 hydr
35	60.5	14.5	589	2	B38128	epithelin/granulin
36	60.5	14.5	825	2	S55060	fertilin alpha-II
37	60.5	14.5	905	2	S55059	fertilin alpha-I -
38	60.5	14.5	1101	2	T16840	hypothetical prote
39	60.5	14.5	2318	2	S45306	notch 3 protein -
40	60	14.4	131	1	KRSHA3	keratin high-sulfu
41	60	14.4	375	1	A60004	matrix protein - m
42	60	14.4	375	1	MFNZMS	matrix protein - m
43	60	14.4	1607	1	MMMSB2	laminin gamma-1 ch
44	60	14.4	2150	2	T32497	hypothetical prote
45	59.5	14.3	372	2	A42778	agglutinin precurs

## ALIGNMENTS

## RESULT 1

JC7188

REIC protein - human

C;Species: Homo sapiens (man)

C;Date: 04-Mar-2000 #sequence\_revision 04-Mar-2000 #text\_change 11-May-2000

C;Accession: JC7188

R;Tsugi, T.; Miyazaki, M.; Sakaguchi, M.; Inoue, Y.; Namba, M.

Biochem. Biophys. Res. Commun. 268, 20-24, 2000

A;Title: A REIC gene shows down-regulation in human immortalized cells and human tumor

A;Reference number: JC7188; MUID:20119095; PMID:10652205

A;Accession: JC7188

A;Molecule type: mRNA

A;Residues: 1-350

A;Cross-references: UNIPARC:UPI0000179471; DDBJ:AB034203

A;Experimental source: heart

C;Comment: This protein is a secreted glycoprotein for head induction in amphibian emb

C;Genetics:

A;Gene: reic

C;Superfamily: human REIC protein

# SCORE Search Results Details for Application 10713567 and Search Result us-10-713-567-6\_copy\_7\_77.rup.

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OM protein - protein search, using sw model

Run on: June 28, 2006, 00:22:07 ; Search time 191 Seconds  
(without alignments)  
343.854 Million cell updates/sec

Title: US-10-713-567-6\_COPY\_7\_77  
Perfect score: 416  
Sequence: 1 CDKDSQCGGGMCCAIVSIWVK.....TCPCLPGLACLRTSFNRFIC 71

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 2849598 seqs, 925015592 residues

Total number of hits satisfying chosen parameters: 2849598

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : UniProt\_7.2:\*  
1: uniprot\_sprot:\*  
2: uniprot\_trembl:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result		%	Query				
No.	Score	Match	Length	DB	ID	Description	
1	416	100.0	108	2	Q6ISR0_HUMAN	Q6isr0 homo sapien	
2	404	97.1	107	1	PROK2_RAT	Q8r413 rattus norv	
3	404	97.1	107	2	Q50E37_9MURI	Q50e37 arvicanthis	
4	404	97.1	107	2	Q50E38_9MURI	Q50e38 arvicanthis	

5	395.5	95.1	129	1	PROK2_HUMAN	Q9hc23	homo sapien
6	395.5	95.1	129	2	Q53Z79_HUMAN	Q53z79	homo sapien
7	383.5	92.2	128	1	PROK2_MOUSE	Q9qxu7	mus musculu
8	383.5	92.2	128	2	Q50E33_9MURI	Q50e33	arvicanthis
9	383.5	92.2	128	2	Q50E34_9MURI	Q50e34	arvicanthis
10	383.5	92.2	128	2	Q6V8J7_RAT	Q6v8j7	rattus norv
11	381	91.6	108	2	Q863H4_BOVIN	Q863h4	bos taurus
12	361	86.8	128	2	Q863H5_BOVIN	Q863h5	bos taurus
13	295	70.9	104	2	Q2XXR8_VARVA	Q2xxr8	varanus var
14	291	70.0	104	2	Q2XXR7_VARVA	Q2xxr7	varanus var
15	289	69.5	81	1	VPRA_DENPO	P25687	dendroaspis
16	278	66.8	102	2	Q4SR12_TETNG	Q4sr12	tetraodon n
17	264	63.5	105	1	PROK1_HUMAN	P58294	homo sapien
18	264	63.5	105	2	Q5VWD4_HUMAN	Q5vwd4	homo sapien
19	263	63.2	105	2	Q8TC69_HUMAN	Q8tc69	homo sapien
20	259	62.3	105	1	PROK1_RAT	Q8r414	rattus norv
21	256	61.5	81	2	Q3ZFI2_BOVIN	Q3zfi2	bos taurus
22	253	60.8	81	2	Q8K457_MOUSE	Q8k457	mus musculu
23	238	57.2	86	2	Q50E35_9MURI	Q50e35	arvicanthis
24	238	57.2	86	2	Q50E36_9MURI	Q50e36	arvicanthis
25	223	53.6	82	2	Q2TBS7_BOVIN	Q2tbs7	bos taurus
26	221.5	53.2	96	1	BV8_BOMVA	Q9pw66	bombina var
27	221.5	53.2	96	2	Q8JFQ0_BOMMX	Q8jfq0	bombina max
28	217.5	52.3	96	2	Q5W280_BOMOR	Q5w280	bombina ori
29	210.5	50.6	96	2	Q8JFE6_BOMMX	Q8jfe6	bombina max
30	209.5	50.4	96	2	Q8JFX9_BOMMX	Q8jfx9	bombina max
31	209.5	50.4	96	2	Q8JFY1_BOMMX	Q8jfy1	bombina max
32	207	49.8	96	2	Q8JFY0_BOMMX	Q8jfy0	bombina max
33	202.5	48.7	96	2	Q8JFX8_BOMMX	Q8jfx8	bombina max
34	200	48.1	106	2	Q4RVU3_TETNG	Q4rvu3	tetraodon n
35	198.5	47.7	96	2	Q8JFY2_BOMMX	Q8jfy2	bombina max
36	122.5	29.4	124	2	Q56R10_PENMO	Q56r10	penaeus mon
37	111.5	26.8	221	1	DKK4_MOUSE	Q8vej3	mus musculu
38	110	26.4	96	2	Q8UUX3_CHICK	Q8uux3	gallus gall
39	105.5	25.4	256	2	Q5EHU6_GECJA	Q5ehu6	gecko japon
40	103	24.8	104	2	Q56R11_PACLE	Q56r11	pacifastacu
41	103	24.8	272	1	DKK1_MOUSE	O54908	mus musculu
42	103	24.8	272	2	Q80UL5_MOUSE	Q80ul5	m dickkopf
43	101	24.3	39	2	Q50E61_9MURI	Q50e61	arvicanthis
44	100.5	24.2	224	1	DKK4_HUMAN	Q9ubt3	homo sapien
45	100.5	24.2	224	2	Q3KNX0_HUMAN	Q3knx0	homo sapien

## ALIGNMENTS

## RESULT 1

## Q6ISR0\_HUMAN

ID Q6ISR0\_HUMAN PRELIMINARY; PRT; 108 AA.

AC Q6ISR0;

DT 10-MAY-2005, integrated into UniProtKB/TrEMBL.

DT 10-MAY-2005, sequence version 1.

DT 21-FEB-2006, entry version 6.

DE Prokineticin 2.

GN Name=PROK2;

OS Homo sapiens (Human).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;

OC Homo.

OX NCBI\_TaxID=9606;

RN [1]